(b) comparing the expression of said gene(s) in the first sample to expression of said gene in a second sample; wherein said comparison is used to diagnose breast cancer.

33. (New) The method of claim 32, wherein said second sample is from said first individual.

34. (New) The method of claim 33, wherein said first sample is breast tissue.

35. (New) The method of claim 33, wherein said second sample is breast tissue.

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36. (New) The method of claim 33, wherein said second sample is cancerous tissue.

37. (New) The method of claim 32, wherein said second sample is from a second individual.

38. (New) The method of claim 37, wherein said first sample is breast tissue.

39. (New) The method of claim 37, wherein said second sample is breast tissue.

40. (New) The method of claim 37, wherein said second sample is cancerous tissue.

41. (New) The method of claim 32, wherein said gene is the gene disclosed in Figure 1 or Figure 2.

42. (New) The method of claim 32, wherein said gene encodes BCR4.

43. (New) The method of claim 32, wherein said expression is measured using a labeled nucleic acid probe.

44. (New) The method of claim 32, wherein said expression is measured utilizing a biochip comprising the sequence disclosed in Figure 1 or Figure 2.

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45. (New) A method for determining the prognosis of an individual with breast cancer comprising determining the expression of a gene at least 75% identical to the sequence disclosed in Figure 1 or Figure 2 in a sample, wherein the expression of the gene is used to determine the prognosis of the individual.

46. (New) The method of claim 45, wherein said gene is the sequence disclosed in Figure 1 or Figure 2.

47. (New) The method of claim 45, wherein said gene encodes BCR4.

48. (New) The method of claim 45, wherein said expression is measured using a labeled nucleic acid probe.

49. (New) The method of claim 45, wherein said expression is measured utilizing a biochip comprising the sequence disclosed in Figure 1 or Figure 2.